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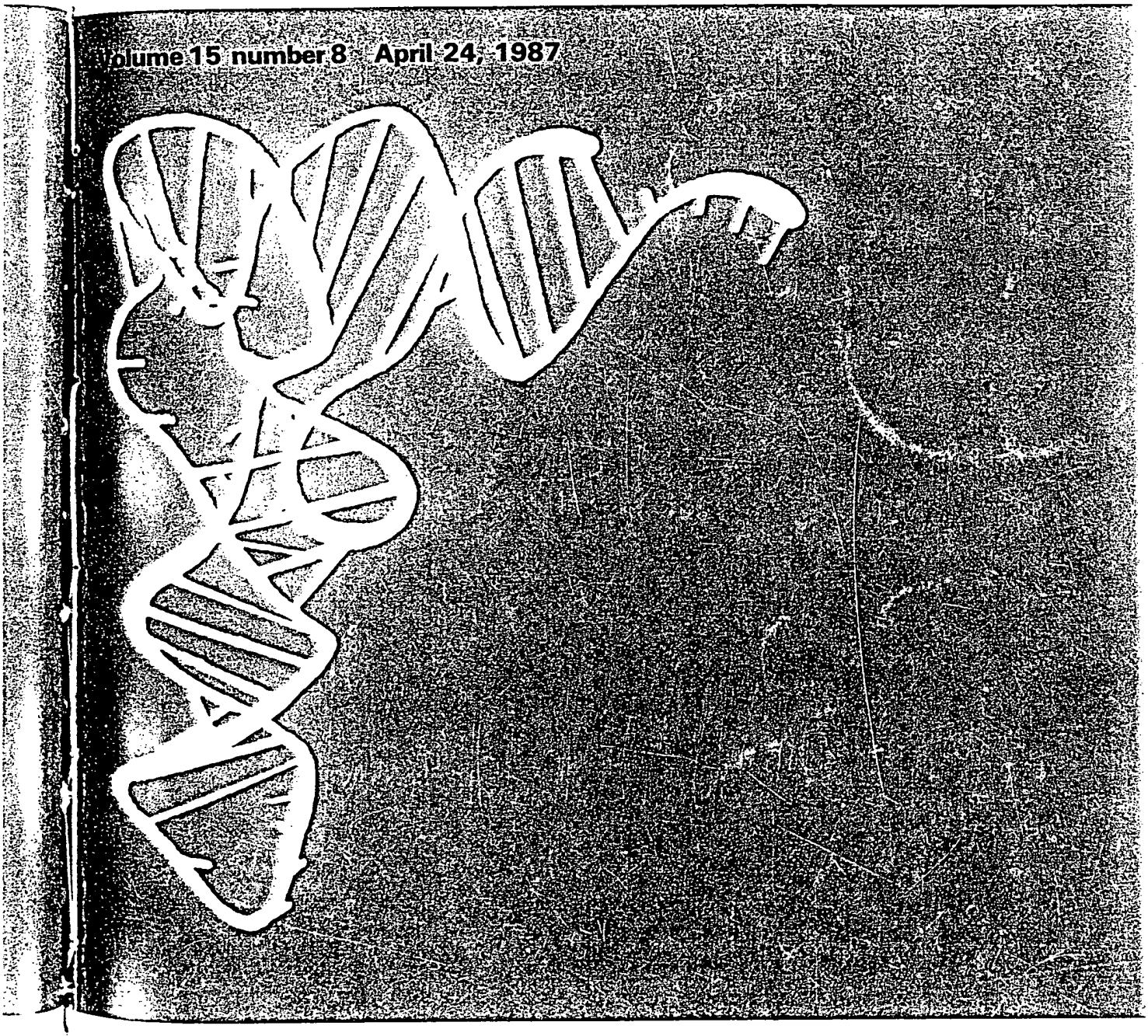

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DNA sequences for typical ribosomal gene spacers from *Xenopus laevis* and *Xenopus borealis*

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We have determined a few short DNA sequences that had not been previously reported from the X. laevis ribosomal gene spacer and about 3 kb of previously unreported sequence from the X. borealis spacer. For the convenience of other workers, we have compiled our data with other published reports so that, for the first time, one can refer to a typical, complete sequence for each of these spacers.

For both spacers, the sequence is shown from the C in the HindIII-recognition site at the 3' end of the 28S rRNA (nucleotide 1) to the transcription start site of the 40S precursor (X. laevis: at nucleotide 3952; X. borealis: 3930). The sequence is complied from the following sources: X. laevis: 1 to 197: (1,2); 190 to 532: (3); 529 to 1474: (2); 1475 to 1664: present work; 1665 to 2910: (2); 2804 to 3051: (1); 3052 to 3634: inferred from restriction data in (4); 3635 to 4000: (1,2). X. borealis: 1 to 453: (3); 454 to 3490: present work; 1081 to 1422: inferred from chemical cleavage pattern and restriction analysis; 2000 to 2296: inferred from restriction data; 3385 to 4000: (5). The clones used were pXlr14 in (1,3) and in the present work, pXl108 in (2,4), and pXbr101A in (5) and in the present work.

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                10        20        30        40        50        60        70        80        90       100
                 |         |         |         |         |         |         |         |         |         |
First nt.
   +1   CTTTTGTCGG AAGGAGCAGG CCGGAAGGGC GCCCCCGCCG CCGGCCGGCG CGACGTCCCG TCCGCCCTCC CCGGCCTCCC GCCGCGCTCC CCTTTCCGCG
 +101   GGGGGGAGAG AGCGGCGGCG GGGCGGGGGG GAGGCGGCCG GGCGACCGCC GCCGGCCCGG GGACCGTCCC GTCCCCCGGC CTCTCCCGCA GGAAGGGGGC
 +201   CGAAGGCCCC TTCGGCCCCC GCACCCCCCC TCCCTCCCGC CGGGGGAGGC CTGACTTGCA GGCCCGCCGC GGGACCCCTC CCGGGGAGCG GGGGGGGGGG
 +301   GACTCTGCGC CCCGCCGACC CACGGCGGGC CTCGGGCCCC TTGCAAGCCC CAGCCGCGGG CCCGTATGCG GGGAGGGCCC CGCCGCCCTC TGGCGCCGGC
 +401   AGGACGGCCG GGGGGGGGGG GCGCGCGGGA GCGACCGAGC GGAGGGGGGG GGGCTTAAGG GTCCGCTGCC CCCGTCCGCA TCCCTCCCCG GGGCTTAAGG
 +501   GCCGCTGCCC GGTCGGGGGC ACCCTCCCCG GGGCTTAAGG GTCGGCGGCC CCCATCCCTC CCCGGGGCTT AAGGGTCGGC GGCCCCCATC CCTCCCCGGG
 +601   GCTTAAGGGC CGGCTGCCCC CATCCCTCCC TGGCCGGGTT AGCACGNGGG CGCTGCCCGG GGGTCCCCGC TGAAGAGGGG GGCGAGAGAA TGAAGAGGTG
 +701   AAGAAAAAAT CTGAGCCGGG GCCGCGGGGG GCCCCAGGGG GGCGGCTCCC GGGGTCCCCC CGGCGAAGAG GGGCCCATTG GGAGGCAGGG GACCCGATTC
 +801   GGGGTCGGGG CCCCGGGGGT GCCCGCTAAG GGGCCCCGGG GGCCCCTCCC GGCGAAGAGG GGCCCATTGG GAGGCAGGGG ACCCGATTCG GGGTCGGGGC
 +901   CCCGGGGGTG CCCGCGGGGG CCCCGGGGGG CGGCTTCCCG GGGTCCCCCC GGCGAAGAGG GGCCCATTCG GAGCCAGGGG ACCCGATTCG GGGTCGGGGC
+1001   CCCGGGGGTG CCCGCGGGGG CCCCGGGGGG CGGCTTCCCG GGGTCCCCCC GGCGAAGAGG GGCCCATTCT GAGCCAGGGG ACCCGATTCG GGGTCGGGGC
+1101   CCCGGGGGTG CCCGCGGGGG CCCCGGGGGG CGGCTTCCCG GGGTCCCCCC GGCGAAGAGG GGCCCATTCT GAGCCAGGGG ACCCGATTCG GGGTCGGGGC
+1201   CCCGGGCCCC GCGGGGGCCC CGGGGGCGGG CTTCCCGGGG TCCCCCCGGC GAAGAGGGGC CCATTCTGAG CCAGGGGACC CGATTCGGGG TCGGGGCCCC
+1301   GGGGGTGCCC GCGGGGGCCC CGGGGCGGGC TCCCGGGCTC CCCCCGGCGA AGAGGGGCCC ATGGGGAGGC AGGGGACCCG ATTCGGGGTC GGGGCCCCGG
+1401   GGGTGCCCGC TAAGGGGCCC CGGGGGGCGG CTCCCGGGGT CCCCCCGGCG AAGAGGGGGC AAGAGGGAAG GGGTGGGAGA GGTAGAGACA AGACAGAGGC
+1501   GGAAAAAACC CTAAGAAAAA AAAAAAATCC CCAGCCGGGC CACCGGGGGG CGCCGCCGGG GGCCCGGGGC GCTGACCAGG GGTCCCCCGC TGAAGAGGGG
+1601   GCGAGAGGGG CGAAGAAAAC CGGAAGAAAT ACCCAGCCGG GCCACCGGGG GGCGCCGCGG AGCGCCCCCT GGAAGTCCCG ATGAGGACGG ATCCGCCCGG
+1701   CCGGGCCCGG CCGGAGTTCC CAGGGGCCTG GGGAGAGGAG CCGGCAGCCC GGCCTCTCGG GCCCCCCGCA CGACGCTGCC ATGCTACGCC TTTTTGGCAT
+1801   GTGCCGGCAG GATTGTAGGG AGCGGCCTCT CGGGAGCCCT GGCCCGGAAG TCCCCGCCGG GGGACCTGGG GCCGGCCCCA GCCCGACCGG GAGTTCCAGG
+1901   AGCTCGGGCA GGGGGAGCAG GCTCGTCCCC CTGCCTGCGG GGGACCTGGG GCCGGCCCCA GCCCCACCGG GAGTTCCAGG AGCTCGGGCA GGGGGAGCAG
+2001   GCTCGTCCCC CTGCCCTGCA GCCCGACCGG GAGTTCCAGG AGCTCGGGCA GAGGGAGCAG GCTCGTCCCC CTGCCCTGCG GGGGACCTGG GGCCGGCCCC
+2101   AGCCCCACCG GGAGTTCCAG GAGCTCGGGC AGGGGGAGCA GGCTCGTCCC CCTGCCCTGC AGCCCGACCG GGAGTTCCAG GAGCTCGGGC AGAGGGAGCA
+2201   GGCTCGTCCC CCTGCCCTGC GGGGGACCTG GGGACGGCCC CAGCCCGACC GGGAGTTCCA GGAGCTCGGG CAGAGGGAGC AGGCTCGTCC CCCTGCCCTG
+2301   CGGGGGACCT GGGGACGGCC CCAGCCCGAC CGGGAGTTCC AGGAGCTCGG GCAGAGGGAG CAGGCTCGTC CCCCTGCCCT AGGAGCTCGG GCAGGGGGAG
+2401   CAGGAGCTCG GCAGGGGGAG CAGGCTCGTC CCCCTGCCCT GCAGCCCGAC CGGGAGTTCC AGGAGCTCGG GCAGAGGGGA GCAGGCTCGT CCCCTGCCCT
+2501   GCGGGGGACC TGGGGACGGC CCCAGCCCGA CCGGGAGTTC CAGGAGCTCG GGCAGAGGGA GCAGGCTCGT CCCCCTGCCC TGCAGCCCGA CCGGGAGTTC
+2601   CAGGAGCTCG GGCAGAGGGA GCAGGCTCGT CCCCCTGCCC TGCGGGGGAC CTGGGCCGGC CCCAGCCCCA CCGGGAGTTC CAGGAGCTCG GGCAGGGGGA
+2701   GCAGGCCCGT CCCCCTGCCC AGGGGCGAAG AAAACCGGGA GAAATACCCA GCCGGCCAC CGGGAGGCGC CGCGGAGCGC CCCCTGGAAG TCCCGATGAG
+2801   GACGGATCCG CCCGGCCGGG CCCGGCCGGA GTTCCCAGGG GCCTGGGGAG AGGAGCCGGC AGCCCGGCCT CTCGGGCCCC CCGCACGGCG CTGCCATGCT
+2901   ACGCCTTTTT GGCATGTGCC GGCAGGATTG TAGGGAGCGG CCTCTCGGGA GCCCTGGCGC CCAAGTTCCC GCCGGGGACC CCGGGCCGGC CCCAGCCCGA
+3001   CCGGGAGTTC CAGGAGCTCG GGCAGGGGGA GCAGGCTCGT CCCCCTGCCC TGCGGGGGAC CTGGGCCGGC CCCCAGCCCC ACCGGGAGTT CCAGGAGCTC
+3101   GGGCAGAGGG AGCAGGCTCG TCCCCCTGCC CTGCAGCCCG ACCGGGAGTT CCAGGAGCTC GGGCAGAGGG AGCAGGCTCG TCCCCCTGCC CTGCGGGGGA
+3201   CCCGGGGCCG GCCCCAGCCC CACCGGGAGT TCCAGGAGCT CGGGCAGAGG GAGCAGGCTC GTCCCCCTGC CCTGCGGGGG ACCCGGGGCC GGCCCCAGCC
+3301   CCACCGGGAG TTCCAGGAGC TCGGGCAGAG GGAGCAGGCT CGTCCCCCTG CCCTGCAGCC CGACCGGGAG TTCCAGGAGC TCGGGCAGAG GGAGCAGGCT
+3401   CGTCCCCCTG CCCTGCGGGG GACCCGGGGC CGGCCCCAGC CCCACCGGGA GTTCCAGGAG CTCGGGCAGA GGGAGCAGGC TCGTCCCCCT GCCCTGCAGC
+3501   CCGACCGGGA GTTCCAGGAG CTCGGGCAGA GGGAGCAGGC TCGTCCCCCT GCCCTGCGGG GGACCCGGGG CCGGCCCCAG CCCCACCGGG AGTTCCAGGA
+3601   GCTCGGGCAG AGGGAGCAGG CTCGTCCCCC TGCCCTGCAG CCCCACCGGG AGTTCCAGGA GCTCGGGCAG GGGGAGCCGG CTCGTCCCCC GGCACCGGAG
+3701   GTCCCCGGGC CCTTTGGCGC CCGTTTTTTC GCAAAGTGCG GCGCCCGCGG GGACTTGCTC GGCCGGGCCG GGCCCCGGCG GCCCCGGGGC CCCGGGGCCC
+3801   TCCCGCGGAG GCCCCGATGA GGACGGATTC GCCCGGCCCG CCCCGGCCGG AGTTCCGGGA GCCCGGGGAG AGGAGCCGGC GGCCCGGCCT CTCGGGCCCC
+3901   CCGCACGACG CCTCCATGCT ACGCTTTTTT GGCATGTGCG GGCAGGAAGG TAGGGGAAGA CCGGCCCTCG GCGCGACGGG CGCCCGAAAA AAGGACCGGG
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FIGURE 1: A typical intergenic spacer region from the ribosomal DNA of Xenopus laevis.

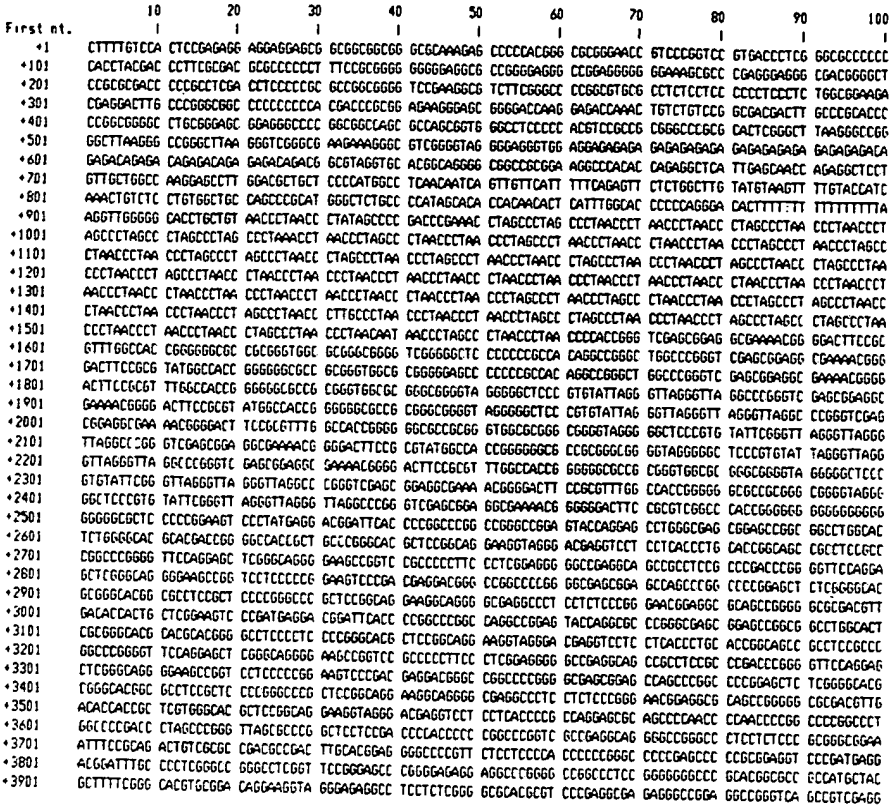

FIGURE 2: A typical intergenic spacer region from the ribosomal DNA of Xenopus borealis.

Partial sequences of spacers from other clones can be found in references (6-10). The sequence of the X. laevis 40S coding region, up to the 3′ end of the 28S sequence, can be assembled from references (7,11,12, and 13).

REFERENCES

1. Sollner-Webb, B. and Reeder, R.H. (1979) Cell 18, 485-499.
2. Moss, T., Boseley, P.G., and Birnstiel, M.L. (1980) Nucl. Acids Res. 8, 467-485.
3. Labhart, P. and Reeder, R.H. (1986) Cell 45, 431-443.
4. Boseley, P., Moss, T., Maechler, M., Portmann, R., and Birnstiel, M. (1979) Cell 17, 19-31.
5. Furlong, J.C., Forbes, J., Robertson, M., and Maden, B.E.H. (1983) Nucl. Acids Res. 11, 8183-8196.
6. Bach, R., Allet, B., and Crippa, M. (1981) Nucl. Acids Res. 9, 5311-5330.
7. Maden, B.E.H., Moss, M., and Salim, M. (1982) Nucl. Acids Res. 10, 2387-2398.
8. LaVolpe, A., Taggart, M., McStay, B., and Bird, A. (1983) Nucl. Acids Res. 11,5361-5380.
9. McStay, B. and Bird, A. (1983) Nucl. Acids Res. 11, 8167-8181.
10. Morgan, G.T., Roan, J.G., Bakken, A.H., and Reeder, R.H. (1984) Nucl. Acids Res. 12, 6043-6052.
11. Salim, M., and Maden, B.E.H. (1981) Nature 291, 205-208.
12. Hall, L.M.C. and Maden, B.E.H. (1980) Nucl. Acids Res. 8, 5993-6005.
13. Ware, V.C., Tague, B.W., Clark, C.G., Gourse, R.L., Brand, R.C., and Gerbi, S.A. (1983) Nucl. Acids Res. 11, 7795-7817.

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We thank
probes, Drs A.

REFERENCES
1. Carle,G.F.,
2. Snell,R.G.